



## SEQUENCE LISTING

<110> Kilian, Andrzej  
Bowtell, David

<120> VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES  
THEREOF

<130> 191106.407C1

<140> 09/502,424

<141> 2000-02-11

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<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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272  
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 Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile  
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 Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln  
 660 665 670  
 Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala  
 675 680 685  
 Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile  
 690 695 700  
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln  
 705 710 715 720  
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser  
 725 730 735  
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu  
 740 745 750  
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser  
 755 760 765  
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe  
 770 775 780  
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys  
 785 790 795 800  
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu  
 805 810 815  
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp  
 820 825 830  
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His  
 835 840 845  
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro  
 850 855 860  
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro  
 865 870 875 880

FMS  
 1  
 1

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala  
885 890 895

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu  
900 905 910

Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala  
915 920 925

Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg  
930 935 940

Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp  
945 950 955 960

Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile  
965 970 975

Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro  
980 985 990

Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile  
995 1000 1005

Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala  
1010 1015 1020

Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu  
1025 1030 1035 1040

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg  
1045 1050 1055

His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln  
1060 1065 1070

Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu  
1075 1080 1085

Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
1090 1095 1100

<210> 5  
<211> 884  
<212> PRT  
<213> Homo sapiens

<400> 5  
Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu  
1 5 10 15

Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn

20 25 30  
 Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg  
 35 40 45  
 Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val  
 50 55 60  
 Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn  
 65 70 75 80  
 Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn  
 85 90 95  
 Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly  
 100 105 110  
 Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val  
 115 120 125  
 Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe  
 130 135 140  
 Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys  
 145 150 155 160  
 Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys  
 165 170 175  
 Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn  
 180 185 190  
 Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser  
 195 200 205  
 Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr  
 210 215 220  
 Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr  
 225 230 235 240  
 Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile  
 245 250 255  
 Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser  
 260 265 270  
 His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile  
 275 280 285  
 Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys  
 290 295 300  
 Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Ser Leu Pro  
 305 310 315 320  
 Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu

325 330 335  
 Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His  
 340 345 350  
 Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu  
 355 360 365  
 Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr  
 370 375 380  
 Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp  
 385 390 395 400  
 Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu  
 405 410 415  
 Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn  
 420 425 430  
 Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu  
 435 440 445  
 Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe  
 450 455 460  
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys  
 465 470 475 480  
 Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile  
 485 490 495  
 Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg  
 500 505 510  
 Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys  
 515 520 525  
 Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met  
 530 535 540  
 Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg  
 545 550 555 560  
 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn  
 565 570 575  
 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp  
 580 585 590  
 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val  
 595 600 605  
 Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr  
 610 615 620  
 Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile

625                      630                      635                      640  
 Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys  
                                  645                      650                      655  
 Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe  
                                  660                      665                      670  
 Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu  
                                  675                      680                      685  
 Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys  
                                  690                      695                      700  
 Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe  
 705                                   710                      715                      720  
 Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser  
                                  725                      730                      735  
 Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile  
                                  740                      745                      750  
 Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr  
                                  755                      760                      765  
 Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp  
                                  770                      775                      780  
 His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp  
 785                                   790                      795                      800  
 Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln  
                                  805                      810                      815  
 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp  
                                  820                      825                      830  
 Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu  
                                  835                      840                      845  
 Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu  
                                  850                      855                      860  
 Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile  
 865                                   870                      875                      880  
 His Ile Val Asn

<210> 6  
 <211> 13  
 <212> DNA  
 <213> Homo sapiens  
 <220>



<221> intron  
 <222> (8)..(13)  
 <223> First six bases of Y intron

<400> 6  
 ccaggtgggc ctc

13

<210> 7  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (1)..(7)  
 <223> Last seven bases of intron Y

<400> 7  
 gcaggtgtcc tgcc

14

<210> 8  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (8)..(14)  
 <223> First 7 bases of Intron 1

<400> 8  
 aaagagggtg gctg

14

<210> 9  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (1)..(7)  
 <223> Last 7 bases of Intron 1

<400> 9  
 aacagaagcc gagc

14

<210> 10  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (8)..(14)  
 <223> First 7 bases of Intron Alpha

<400> 10

INS  
 A1

tgtcaagggtg gatg

14

<210> 11  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (1)..(7)  
 <223> Last 7 bases of Intron Alpha

<400> 11  
 cccccaggac aggc

14

<210> 12  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (8)..(14)  
 <223> First 7 bases of Intron Beta

<400> 12  
 gagccacgtc tcta

14

<210> 13  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (1)..(7)  
 <223> Last 7 bases of Intron Beta

<400> 13  
 ggggcaagtc ctac

14

<210> 14  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (8)..(14)  
 <223> First 7 base of Intron 2

<400> 14  
 actccaggtg agcg

14

<210> 15  
 <211> 14  
 <212> DNA

IMS  
 14

<213> Homo sapiens

<220>

<221> modified base

<222> (1)..(7)

<223> Wherein N is any nucleotide

<220>

<221> intron

<222> (1)..(7)

<223> Last 7 bases of Intron 2

<400> 15

nnnnnnncta tgcc

14

<210> 16

<211> 173

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (8)..(166)

<223> Full Sequence of Intron 3

<400> 16

aacgcagccg aagaaaacat ttctgtcgtg actcctgcgg tgcttgggtc gggacagcca 60  
gagatggagc caccgcgag accgtcgggt gtgggcagct ttccggtgtc tcctgggagg 120  
ggagttgggc tgggcctgtg actcctcagc ctctgttttc cccagggat gtc 173

<210> 17

<211> 46

<212> PRT

<213> Homo sapiens

<400> 17

Thr Ala Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly  
1 5 10 15

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly  
20 25 30

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
35 40 45

<210> 18

<211> 104

<212> DNA

<213> Homo sapiens

<220>

<223> Intron Y

<400> 18

ggctccccg ggtcggcgt ccggctgggg ttgagggcgg ccggggggaa ccagcgacat 60  
gcggagagca gcgcaggcga ctcagggcgc ttccccgcga ggtg 104

<210> 19  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Reding Frame One of Intron Y

<400> 19  
 Gly Leu Pro Gly Val Gly Val Arg Leu Gly Leu Arg Ala Ala Gly Gly  
 1 5 10 15  
 Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro  
 20 25 30

Arg Arg

<210> 20  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Reading Frame Two of Intron Y before termination  
 Codon

<400> 20  
 Ala Ser Pro Gly Ser Ala Ser Gly Trp Gly  
 1 5 10

<210> 21  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Reading Frame Two of Intron Y after termination  
 Codon

<400> 21  
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr  
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly  
 20

<210> 22  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<220>

<223> Reading Frame Three of Intron Y

<400> 22

Pro Pro Arg Gly Arg Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu  
1 5 10 15

Pro Ala Thr Cys Gly Glu Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro  
20 25 30

Gln Val

<210> 23

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<223> Intron 1

<400> 23

gtggctgtgc tttggtttaa cttccttttt aaccagaa

38

<210> 24

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 1 Translation

<400> 24

Val Ala Val Leu Trp Phe Asn Phe Leu Phe Asn Gln Lys  
1 5 10

<210> 25

<211> 36

<212> DNA

<213> Homo sapiens

<220>

<223> Intron Alpha

<400> 25

gtggatgtga cgggcgcgta cgacaccatc ccccag

36

<210> 26

<211> 12

<212> PRT

<213> Homo sapiens

<220>

<223> Intron Alpha Translation

<400> 26

Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln  
 1 5 10

<210> 27  
 <211> 182  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Intron Beta

<400> 27  
 gtctctacct tgacagacct ccagccgtac atgcgacagt tcgtgggtca cctgcaggag 60  
 accagccgc tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc 120  
 agtggcctct tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc 180  
 aa 182

<210> 28  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Intron Beta Translation

<400> 28  
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala  
 1 5 10 15  
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln  
 20 25 30  
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu  
 35 40 45  
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys  
 50 55 60

<210> 29  
 <211> 226  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Intron 2

<400> 29  
 gtgagcgcac ctggccggaa gtggagcctg tgcccggctg gggcagggtgc tgcctgcaggg 60  
 ccgttgctgc cacctctgct tccgtgtggg gcaggcgact gccaatccca aagggtcaga 120  
 tgccacaggg tgcccctcgt cccatctggg gctgagcaca aatgcattct tctgtgggag 180  
 tgagggtgcc tcacaacggg agcagttttc tgtgctattt tggtaa 226

<210> 30  
 <211> 159  
 <212> DNA

<213> Homo sapiens

<220>

<223> Intron 3

<400> 30

ccgaagaaaa catttctgtc gtgactcctg cgggtgcttg gtcgggacag ccagagatgg 60  
agccaccccg cagaccgtcg ggtgtgggca gctttccggt gtctcctggg aggggagttg 120  
ggctgggcct gtgactcctc agcctctgtt ttccccag 159

<210> 31

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 3 Translation

<400> 31

Ala Glu Glu Asn Ile Ser Val Val Thr Pro Ala Val Leu Gly Ser Gly  
1 5 10 15

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe  
20 25 30

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
35 40

<210> 32

<211> 262

<212> DNA

<213> Homo sapiens

<220>

<223> Intron X. Complete length unknown

<400> 32

gacagtcacc agggggggttg accgocggac tgggcgtccc cagggttgac tataggacca 60  
ggtgtccagg tgccctgcaa gtagaggggc tctcagaggc gtctggctgg catgggtgga 120  
cgtggccccc ggcatggcct tctgcgtgtg ctgccgtggg tgccctgagc cctcactgag 180  
tcggtggggg cttgtggctt cccgtgagct tccccctagt ctgtgtctg gctgagcaag 240  
cctcctgagg ggctctctat tg 262

<210> 33

<211> 218

<212> DNA

<213> Homo sapiens

<220>

<223> Partial Sequence of Genomic Intron (approximately 2.7 kb)

<400> 33

gtggctgtgc tttggtttaa cttccttttt aaccagaagt gcgtttgagc cccacatttg 60  
gtatcagctt agatgaaggg ccggaggag gggccacggg acacagccag ggccatggga 120  
cggcgcccac ccatttgtgc gcacagttag gtggccgagg tgccggtgcc tccagaaaag 180

cagcctgggg gtgtaggggg agctcctggg gcagggac

218

<210> 34

<211> 2031

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1767)..(1769)

<223> Wherein N is A, C, G or T

<220>

<223> N-Terminal Truncated Telomerase

<400> 34

atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60  
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120  
cgcgggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180  
gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgtcctgcct gaaggagctg 240  
gtggcccagag tgctgcagag gctgtgcgag cgcggcgcca agaactgtgt ggcttcggc 300  
ttcgcgctgc tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360  
agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgtg ggggctgctg 420  
ctgcgcgcgc tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480  
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgt 540  
gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600  
cgggcctgga accatagcgt cagggaggcc ggggtcccc tgggcctgcc agccccgggt 660  
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gccaggcgt 720  
ggcgtgccc cgtgacccga gcggacccc gttgggcagg ggtcctgggc ccaccgggc 780  
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840  
gaagccacct ctttggaggg tgcgtctctt ggcacgcgcc actcccacc atcctgtggc 900  
cgccagcacc acgcggggcc cccatccaca tgcggccac cacgtccctg ggacacgct 960  
tgtcccccg tgtacccga gaccaagcac ttctctact cctcaggcga caaggagcag 1020  
ctgcggccct ccttctact cagctctctg aggccagcc tgactggcgc tcggaggctc 1080  
gtggagacca tctttctggg ttccaggccc tgatgccag ggactcccc caggttgccc 1140  
cgctgcccc agcgtactg gcaaagtgcg ccctgtttc tggagctgct tgggaaccac 1200  
gcgcagtgcc cctacgggtt gctcctcaag acgactgcc cgctgcgagc tgcggtcacc 1260  
ccagcagccg gtgtctgtgc ccgggagaag ccccgaggct ctgtggcggc ccccgaggag 1320  
gaggacacag accccgctc cctggtgcag ctgctcgcgc agcacagcag cccctggcag 1380  
gtgtacggct tcgtgcgggc ctgectgcgc cggctggtgc cccaggcct ctggggctcc 1440  
aggcacaacg aacgcgcctt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500  
gccaagctct cgctgcagga gctgacgtg aagatgagc tgccggactg cgcttggtg 1560  
cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620  
ctggccaagt tctgcaactg gctgatgagt gtgtacgtcg tgcagctgct caggtctttc 1680  
ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740  
tggagcaagt tgcaaagcat tggaaatnng acagtcacca ggggggttga ccgccggact 1800  
ggcgctcccc agggttgact ataggaccag gtgtccagg gcccgtgcaag tagaggggct 1860  
ctcagaggcg tctggctggc atgggtggac gtggccccg gcattgcctt ctgcgtgtgc 1920  
tgccgtgggt gccctgagcc ctactgagt cggtaggggc ttgtgcttc ccgtgagctt 1980  
ccccctagtc tgttgtctgg ctgagcaagc ctctgaggg gctctctatt g 2031

<210> 35

<211> 588

<212> PRT

<213> Homo sapiens

<220>



<223> Protein Predicted by SEQ ID NO:34

<400> 35

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575  
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly  
 580 585

<210> 36  
 <211> 2041  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 1; Intron 1 Addition

<400> 36

atgccgcgcg cteccccctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60  
 gtgctgccgc tggccacatt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120  
 cgcggggacc cggcggtttt ccgcgcgtg gtggcccagt gcctggtgtg cgtgccctgg 180  
 gacgcacggc cccccccg cgcctccctc ttccgccagg tgcctgcct gaaggagctg 240  
 gtggcccagag tgctgcagag gctgtgcgag cgcggcgcga agaactgtgt ggcttcggc 300  
 ttgcgcgtgc tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360  
 agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgtg ggggctgctg 420  
 ctgcgcgcgc tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480  
 ctggtggctc ccagctggc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540  
 gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600  
 cgggcctgga accatagcgt cagggaggcc ggggtccccc tgggcctgcc agccccgggt 660  
 gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgccaagag gccacggcgt 720  
 ggcgtgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccaccgggc 780  
 aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840  
 gaagccacct ctttggaggg tgcgctctct ggcacgcgcc actccacccc atcgtgggc 900  
 cgccagcacc acgcggggcc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960  
 tgtccccggg tgtacgccga gaccaagcac ttctctact cctcaggcga caaggagcag 1020  
 ctgcggccct ccttctact cagctctctg aggccagacc tgactggcgc tcggaggctc 1080  
 gtggagacca tctttctggg ttccaggccc tgatgccag ggactccccg caggttgccc 1140  
 cgctgcccc agcgtactg gcaaattgcg cctgtgttc tgagctgct tgggaaccac 1200  
 gcgcagtgcc cctacggggg gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260  
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 gtgtacggct tcgtgcgggc ctgcctgcgc cgctgggtgc ccccgagcct ctggggctcc 1440  
 aggcacaacg aacgcgcgtt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500  
 gccaaactct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggtg 1560  
 cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620  
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 ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740  
 tggagcaagt tgcaaagcat tggaaacaga cagcaactga agaggggtgca gctgcgggag 1800  
 ctgtcggaag cagaggtcag gcagcatcgg gaagccagge ccgcctgct gacgtccaga 1860  
 ctccgcttca tccccagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920  
 ggagccagaa cgttccgcag agaaaagagg gtggctgtgc tttggtttaa cttcctttt 1980  
 aaccagaagc cgagcgtctc acctcgaggg tgaaggcact gttcagcgtg ctcaactacg 2040  
 a 2041

<210> 37  
 <211> 670  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 1; Encoded by SEQ ID NO:36

<400> 37

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125  
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140  
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
 145 150 155 160  
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 165 170 175  
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180 185 190  
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
 195 200 205  
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
 210 215 220  
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260 265 270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575  
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
 580 585 590  
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
 595 600 605  
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe  
645 650 655

Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly  
660 665 670

<210> 38  
<211> 2541  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Truncated Protein 2; Alpha Intron Addition

<400> 38

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gtgctgcgcg tggccacgtt cgtgcgcgcg ctggggcccc agggctggcg gctggtgcag 120  
cgcggggacc cggcggttt ccgcgcgtg gtggccaggt gcctggtgtg cgtgccctgg 180  
gacgcacggc cgcgcgcgcg cgcgcgcgtt ttcgcgcagg tgcctgcct gaaggagctg 240  
gtggcccgag tgctgcagag gctgtgcgag cgcgggcgca agaactgtct ggccttcggc 300  
ttcgcgctgc tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360  
agctacctgc ccaacacggg gaccgacgca ctgcggggga gcggggcggt ggggctgctg 420  
ctgcgcgcgc tgggcgacga cgtgctggtt cacctgctgg cacgctgcgc gctctttgtg 480  
ctggtggctc ccagctgcgc ctaccaggtg tgcgggcgcg cgtgtacca gctcggcgct 540  
gcaactcagg ccgcggcccc gccacacgct actggacccc gaaggcgtct gggatgcgaa 600  
cgggcctgga accatagcgt cagggaggcc ggggtcccc tggcctgcc agccccgggt 660  
gcgaggaggc gcgggggcag tgccagccga agtctgcgt tgcgaagag gccaggcgt 720  
ggcgtgccc ctgagccgga gcggacgccc gttggcagg ggtcctgggc ccaccgggc 780  
aggacgcgtg gaccgagtga ccgtggtttc tgtgtgtgt cacctgccag acccgccgaa 840  
gaagccacct ctttgagggt tgcgtctctt ggcacgcgc actcccacc atcctgtggc 900  
cgccagcacc acgcgggccc cccatccaca tcgcgggcac cagctccctg ggacacgcct 960  
tgtcccccg tgtacgcga gaccaagcac ttcctctact cctcaggcga caaggagcag 1020  
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gtggagacca tctttctggg ttccaggccc tggatgccag ggactcccc caggttgccc 1140  
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gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgtgcgagc tgcggtcacc 1260  
ccagcagccg gtgtctgtgc ccgggagaag ccccagggct ctgtggcggc ccccgaggag 1320  
gaggacacag acccccgtcg cctggtgcag ctgtccgcc agcagcagc cccctggcag 1380  
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc cccaggcct ctggggctcc 1440  
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gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggtg 1560  
cgaggagcc cagggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620  
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ggagccagaa cgttccgcag agaaaagagg gccgagcgct tcacctcgag ggtgaaggca 1980  
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgctctgtg 2040  
ctgggcctgg acgatatcca cagggcctgg cgcaccttgc tgcgtgctgt gcgggcccag 2100  
gaccgcgcgc ctgagctgta ctttgtcaag gtggatgtga cgggcgcgta cgacacatc 2160  
ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aacccagaa cagtaactgc 2220

gtgctgctgt atgcccgtgt ccagaaggcc gcccatgggc acgtccgcaa ggccttcaag 2280  
 agccacgtcc tacgtccagt gccaggggat cccgcagggc tccatcctct ccacgtgct 2340  
 ctgcagcctg tgcacggcg acatggagaa caagctgttt gcggggattc ggcgggacgg 2400  
 gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca cccacgcgaa 2460  
 aaccttcctc aggaacctgg tccgaggtgt ccctgagtat ggctgctggt tgaacttgcg 2520  
 gaagacagtg gtgaacttcc c 2541

<210> 39

<211> 806

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 2; Encoded by SEQ ID NO:38

<400> 39

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
 145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
 195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260 265 270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525



Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575  
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
 580 585 590  
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
 595 600 605  
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
 610 615 620  
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
 625 630 635 640  
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
 645 650 655  
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
 660 665 670  
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg  
 675 680 685  
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
 690 695 700  
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile  
 705 710 715 720  
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
 725 730 735  
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His  
 740 745 750  
 Gly His Val Arg Lys Ala Phe Lys Ser Val Leu Arg Pro Val Pro Gly  
 755 760 765  
 Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu  
 770 775 780  
 Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala  
 785 790 795 800  
 Ala Pro Ala Phe Val Gly  
 805

&lt;211&gt; 3396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; Reference Telomerase; with Intron Alpha and Beta

&lt;400&gt; 40

atgccgcgcg	ctccccctg	ccgagccgtg	cgctccctgc	tgcgcagcca	ctaccgcgag	60
gtgctgccgc	tggccacgtt	cgtgcggcgc	ctggggcccc	agggctggcg	gctggtgcag	120
cgcggggacc	cgcgggcttt	ccgcgcgctg	gtggcccagt	gcctggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgctctgect	gaaggagctg	240
gtggccccgag	tgtgcagag	gctgtgcgag	cgcggcgcga	agaacgtgct	ggccttcggc	300
ttcgcgctgc	tggacggggc	ccgcgggggc	ccccccgagg	ccttcaccac	cagcgtgcgc	360
agctacctgc	ccaacacggt	gacgcagcga	ctgcggggga	gcggggcgctg	ggggctgctg	420
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gccactcagg	cccgggcccc	gccacacgct	agtggacccc	gaaggcgtct	gggatgcgaa	600
cgggcctgga	accatagcgt	cagggaggcc	ggggctcccc	tgggcctgcc	agccccgggt	660
gcgaggaggc	gcgggggcag	tgccagccga	agtctgccgt	tgcccaagag	gcccaggcgt	720
ggcgtgccc	ctgagccgga	gcggaagccc	gttgggcagg	ggtcctgggc	ccaccggggc	780
aggacgcgtg	gaccgagtga	ccgtggtttc	tgtgtggtgt	cacctgccag	acccgccgaa	840
gaagccacct	ctttggaggg	tgcgtctctc	ggcacgcgcc	actccacccc	atccgtgggc	900
cgccagcacc	acgcggggcc	cccatccaca	tgcgggccac	cacgtccctg	ggacacgcct	960
tgccccccg	tgtacgcga	gaccaagcac	ttcctctact	cctcaggcga	caaggagcag	1020
ctgcggccct	ccttctctact	cagctctctg	agccccagcc	tgaactggcg	tcggaggctc	1080
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cgctgcccc	agcgtactg	gcaaagtgcg	ccctgttttc	tggagctgct	tgggaaccac	1200
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ccagcagccg	gtgtctgtgc	ccgggagaag	ccccagggct	ctgtggcggc	ccccgaggag	1320
gaggacacag	acccccgtcg	cctggtgcag	ctgctccgcc	agcacagcag	ccccctggcag	1380
gtgtacgggt	tgcgtcgggc	ctgcctgcgc	cggctggtgc	ccccaggcct	ctggggctcc	1440
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ctggccaagt	tcttgactg	gctgatgagt	gtgtacgtcg	tcgagctgct	caggctcttc	1680
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ggagccagaa	cgttccgcag	agaaaagagg	gccgagcgtc	tcacctcgag	ggtgaaggca	1980
ctgttcagcg	tgctcaacta	cgagcgggcg	cggcgccccg	gcctctgggg	cgctctgtg	2040
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gccagcagtg	gcctcttcga	cgtcttccca	cgcttcatgt	gccaccacgc	cgctgcgcatc	2460
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<210> 41

<211> 3069

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein 3; with Introns Alpha, Beta and  
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<400> 41

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<210> 42

<211> 948

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3; Encoded by SEQ ID NO:41

<400> 42

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 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125  
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140  
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
 145 150 155 160  
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180 185 190  
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
 195 200 205  
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
 210 215 220  
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260 265 270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
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 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
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 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
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 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575  
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
 580 585 590  
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
 595 600 605  
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
 610 615 620  
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
 625 630 635 640  
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
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 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
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 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
 690 695 700  
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 705 710 715 720  
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
 725 730 735  
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His  
 740 745 750  
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp  
 755 760 765  
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser  
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Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu  
 785 790 795 800  
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His  
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 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro  
 820 825 830  
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp  
 835 840 845  
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu  
 850 855 860  
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala  
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 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys  
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 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu  
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 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe  
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&lt;210&gt; 43

&lt;211&gt; 3362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

 <223> Altered C-terminus Protein; with Intron Alpha,  
 Beta and 3

&lt;400&gt; 43

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 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Altered C-terminus Protein; Encoded by SEQ ID  
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 35 40 45  
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 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125  
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140  
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 145 150 155 160  
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 165 170 175  
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180 185 190  
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
 195 200 205  
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
 210 215 220  
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
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 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
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 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
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 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
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 370 375 380  
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 385 390 395 400  
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 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
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 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
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 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575  
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
 580 585 590  
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
 595 600 605  
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
 625 630 635 640  
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
 645 650 655  
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
 660 665 670  
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 675 680 685  
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
 690 695 700  
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile  
 705 710 715 720  
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
 725 730 735  
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His  
 740 745 750  
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp  
 755 760 765  
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser  
 770 775 780  
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu  
 785 790 795 800  
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 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro  
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 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp  
 835 840 845  
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu  
 850 855 860  
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala  
 865 870 875 880  
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys  
 885 890 895  
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu  
 900 905 910  
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe  
 915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser  
 930 935 940  
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe  
 945 950 955 960  
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly  
 965 970 975  
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn  
 980 985 990  
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln  
 995 1000 1005  
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln  
 1010 1015 1020  
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala  
 1025 1030 1035 1040  
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn  
 1045 1050 1055  
 Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met  
 1060 1065 1070  
 Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro  
 1075 1080 1085  
 Gly Arg Gly Val Gly Leu Gly Leu  
 1090 1095

<210> 45  
 <211> 3918  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Protein that lacks Motif A; with Intron Beta

<400> 45  
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 cgcggggacc cggcgcttt ccgcgcgtg gtggcccagt gcctggtgtg cgtgccctgg 180  
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 ctgcgcgcgc tgggcgacga cgtgctggtt cactgctgg cacgctgcgc gctctttgtg 480  
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 gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600  
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aggaacgcgtg gaccgagtgga ccgtgggtttc tgtgtgggtg cacctgccag acccgccgaa 840  
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 gccctgggtg gcacggcttt tgttcagatg ccggcccacg gcctattccc ctggtgcggc 2760  
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 ctggggtcac tcaggacagc ccagacgcag ctgagtcgga agctcccggg gacgacgtg 3300  
 actgccctgg aggcgcgag caaccgcga ctgccctcag acttcaagac catcctggac 3360  
 tgatggccac ccgcccacag ccaggccgag agcagacacc agcagccctg tcacgcccgg 3420  
 ctctacgtcc cagggaggga gggcgggccc acaccaggc ccgcaccgct gggagtctga 3480  
 ggcctgagtg agtggttggc cgaggcctgc atgtccgct gaaggctgag tgtccggtg 3540  
 aggcctgagc gagtgtccag ccaagggtg agtgtccagc acacctgccg tcttcacttc 3600  
 cccacaggct ggcgtcggc tccaccccag ggccagctt tctcaccag gagcccggct 3660  
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 cctcctttg ctttccacc ccaccatcca ggtggagacc ctgagaagga ccctgggagc 3780  
 tctgggaatt tggagtgacc aaaggtgtg cctgtacaca ggcgaggacc ctgcacctgg 3840  
 atgggggtcc ctgtgggtca aattgggggg aggtgctgtg ggagtaaaat actgaatata 3900  
 tgagtttttc agttttga 3918

<210> 46  
 <211> 1120  
 <212> PRT

<213> Homo sapiens

<220>

<223> Protein that lacks Motif A; Encoded by SEQ ID  
NO:45

<400> 46

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
 580 585 590  
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
 595 600 605  
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
 610 615 620  
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
 625 630 635 640  
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
 645 650 655  
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
 660 665 670  
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg  
 675 680 685  
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
 690 695 700  
 Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile  
 705 710 715 720  
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln  
 725 730 735  
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser  
 740 745 750  
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu  
 755 760 765  
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser  
 770 775 780  
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe  
 785 790 795 800  
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys  
 805 810 815  
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu  
 820 825 830  
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp  
 835 840 845  
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His  
 850 855 860  
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro  
 865 870 875 880



Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro  
 885 890 895  
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala  
 900 905 910  
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu  
 915 920 925  
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala  
 930 935 940  
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg  
 945 950 955 960  
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp  
 965 970 975  
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile  
 980 985 990  
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro  
 995 1000 1005  
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile  
 1010 1015 1020  
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala  
 1025 1030 1035 1040  
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu  
 1045 1050 1055  
 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg  
 1060 1065 1070  
 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln  
 1075 1080 1085  
 Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu  
 1090 1095 1100  
 Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
 1105 1110 1115 1120

<210> 47  
 <211> 3033  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein that lacks Motif A; with Introns

## Beta and 2

&lt;400&gt; 47

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cgcggggacc	cggcggtttt	ccgcgcgtg	gtggcccagt	gcctggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgtcctgcct	gaaggagctg	240
gtggcccag	tgctgcagag	gctgtgcgag	cgcggcgoga	agaacgtgct	ggccttcggc	300
ttcgcgctgc	tggacggggc	ccgcgggggc	ccccccgagg	ccttcaccac	cagcgtgcgc	360
agctacctgc	ccaacacggt	gaccgacgca	ctgcggggga	gcggggcgtg	ggggctgctg	420
ctgcgccgcg	tgggcgacga	cgtgctggtt	cacctgctgg	cacgctgcgc	gctctttgtg	480
ctggtggctc	ccagctgcgc	ctaccagggtg	tgcgggcccgc	cgctgtacca	gctcggcgct	540
gccactcagg	ccgggcccc	gccacacgct	agtggacccc	gaaggcgtct	gggatgcgaa	600
cgggcctgga	accatagcgt	cagggaggcc	gggggtcccc	tgggcctgcc	agccccgggt	660
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ccctcgtecc	atctggggct	gagcacaat	gcattctttct	gtgggagtga	gggtgcctca	3000
caacggggagc	agttttctgt	gctatttttg	taa			3033

&lt;210&gt; 48

&lt;211&gt; 936

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein that lacks Motif A; Encoded by  
SEQ ID NO:47

<400> 48

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val

260 265 270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr

565 570 575  
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
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 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
 595 600 605  
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
 610 615 620  
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
 625 630 635 640  
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
 645 650 655  
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
 660 665 670  
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg  
 675 680 685  
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
 690 695 700  
 Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile  
 705 710 715 720  
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln  
 725 730 735  
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser  
 740 745 750  
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu  
 755 760 765  
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser  
 770 775 780  
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe  
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 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys  
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 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu  
 820 825 830  
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp  
 835 840 845  
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His  
 850 855 860  
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro

865 870 875 880  
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro  
                   885                  890                  895  
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala  
                   900                  905                  910  
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu  
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 Glu Val Gln Ser Asp Tyr Ser Arg  
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<210> 49

<211> 3326

<212> DNA

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus;  
 with Introns Beta and 3

<400> 49

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<210> 50  
 <211> 1084  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Protein Lacking Motif A and Altered C-Terminus;  
 Encoded by SEQ ID NO:49

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 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr

115	120	125
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val 130 135 140		
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val 145 150 155 160		
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr 165 170 175		
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly 180 185 190		
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg 195 200 205		
Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg 210 215 220		
Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg 225 230 235 240		
Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp 245 250 255		
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val 260 265 270		
Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala 275 280 285		
Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His 290 295 300		
Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro 305 310 315 320		
Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 325 330 335		
Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro 340 345 350		
Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser 355 360 365		
Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln 370 375 380		
Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His 385 390 395 400		
Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg 405 410 415		
Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln		



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Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu		
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Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe		
	450					455					460						
Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser		
465					470					475					480		
Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser		
			485						490					495			
Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met		
			500					505					510				
Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys		
		515					520					525					
Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe		
	530					535					540						
Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe		
545					550					555					560		
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr		
			565						570					575			
Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His		
			580					585					590				
Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln		
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His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile		
	610					615					620						
Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val		
625					630					635					640		
Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser		
				645					650					655			
Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg		
			660					665					670				
Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg		
	675						680					685					
Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro		
	690					695					700						
Glu	Leu	Tyr	Phe	Val	Lys	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile		
705					710					715					720		
Ile	Lys	Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln		

725										730					735				
Lys	Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser				
			740						745					750					
Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu				
		755						760				765							
Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser				
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Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe				
785					790					795					800				
Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys				
				805					810					815					
Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu				
			820					825					830						
Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp				
		835					840					845							
Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His				
	850					855						860							
Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro				
865					870					875					880				
Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro				
				885					890					895					
Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala				
			900					905					910						
His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu				
		915					920					925							
Glu	Val	Gln	Ser	Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala				
	930					935					940								
Ser	Leu	Thr	Phe	Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg				
945				950						955					960				
Lys	Leu	Phe	Gly	Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp				
				965					970					975					
Leu	Gln	Val	Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile				
			980				985						990						
Leu	Leu	Leu	Gln	Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro				
		995				1000						1005							
Phe	His	Gln	Gln	Val	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	Val	Ile				
	1010					1015						1020							
Ser	Asp	Thr	Ala	Ser	Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	Asn	Ala				

1025                      1030                      1035                      1040  
 Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly  
                          1045                      1050                      1055  
 Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe  
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 Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
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<210> 51  
 <211> 2135  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1871)..(1873)  
 <223> Wherein N is A, C, G or T

<220>  
 <223> N-Terminal Truncated Telomerase (ver. 2); with  
 Intron Y

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<210> 52

<211> 622

<212> PRT

<213> Homo sapiens

<220>

<223> N-Terminal Truncated Telomerase (ver.2); encoded  
by SEQ ID NO:51 and ORF1 of Intron Y

<400> 52

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala

210	215	220
Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 225 230 235 240		
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 245 250 255		
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 265 270		
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 275 280 285		
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295 300		
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 310 315 320		
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 330 335		
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 340 345 350		
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 355 360 365		
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 370 375 380		
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 385 390 395 400		
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 410 415		
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 425 430		
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 435 440 445		
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450 455 460		
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 465 470 475 480		
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 485 490 495		
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 500 505 510		
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe		

515                      520                      525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
     530                      535                      540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
     545                      550                      555                      560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
                     565                      570                      575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
                     580                      585                      590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
                     595                      600                      605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly  
     610                      615                      620

<210> 53

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<223> Splicing Variant of Human Telomerase encoded by  
 Intron Y, ORF2, before the termination codon.  
 SEQ ID NOs: 51,55,59,63,67,71,75,79,83 encode this  
 fragment

<400> 53

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
     1                      5                      10                      15  
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
                     20                      25                      30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
                     35                      40                      45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
     50                      55                      60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala  
     65                      70                      75                      80  
 Ser Gly Trp Gly

<210> 54

<211> 537

<212> PRT

<213> Homo sapiens

&lt;220&gt;

<223> N-Terminal Truncated Telomerase (ver. 2); encoded  
by SEQ ID NO:51, with Y intron, ORF2, after the  
termination codon

&lt;400&gt; 54

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr  
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460  
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525  
 Val Trp Ser Lys Leu Gln Ser Ile Gly  
 530 535

<210> 55  
 <211> 2145  
 <212> DNA  
 <213> Homo sapiens



&lt;220&gt;

&lt;223&gt; Truncated Protein 1 (ver.2); with Introns Y and 1

&lt;400&gt; 55

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atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgcccg tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120
cgcggggacc cggcggtctt ccgcgcgtg gtggcccagt gcctgggtgtg cgtgccctgg 180
gacgcacggc cgtccccgcg cgtccccctc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtctg 360
agaggctgtg cgagcgcggc gcgaagaacg tcttgccctt cggcttcgcg ctgctggacg 420
ggcccccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccacaa 480
cggtgaccga cgcactgcgg gggagcgggg cgtggggggt gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgtcttt tgtgctgggt gctcccagct 600
gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgtgccact caggccccgc 660
ccccgccaca cgctagtga ccccgaggc gtctgggatg cgaacggggc tggaccata 720
gcgtcagggg ggccgggggt cccctggggc tgccagcccc ggggtgcgag aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctcttgg 960
aggtgctgct ctctggcacg cgcactccc acccatccgt gggccgccag caccacgcgg 1020
gcccccatc cacatcgcg ccaccacgtc cctgggacac gccttgccc ccggtgtacg 1080
ccgagaccaa gcacttctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200
tgggttccag gccctggatg ccagggactc ccgcaggtt gccccgcctg cccagcgct 1260
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gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
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gggcctgcct gcgcgggtg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttctcag gaacaccaag aagttcatct ccctggggaa gcattgccaag ctctcgctgc 1620
aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680
ttggtgtgtg tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggccgccc tgctgacgtc cagactccgc ttcaccccca 1980
agcctgacgg gctgcggcgg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gaggttggt gtgctttggt ttaacttct ttttaaccag aagccgagcg 2100
tctcacctcg aggggtgaagg cactgttcag cgtgctcaac tacga 2145

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&lt;210&gt; 56

&lt;211&gt; 704

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Truncated Protein 1 (ver.2); encoded by SEQ ID  
NO:55, with Y Intron ORF1

&lt;400&gt; 56

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Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
  1           5           10           15

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
      20           25           30

```

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
 65 70 75 80  
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
 85 90 95  
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
 100 105 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
 115 120 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 130 135 140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 145 150 155 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
 195 200 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
 210 215 220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
 225 230 235 240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
 245 250 255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 260 265 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu  
675 680 685

Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly  
690 695 700

<210> 57

<211> 619

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2): encoded by SEQ ID  
NO:55, with Intron Y ORF2 after the termination  
codon

<400> 57

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr  
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
 165 170 175  
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
 545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590

Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe Thr Phe Leu  
 595 600 605

Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly  
 610 615

<210> 58

<211> 704

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2); encoded by SEQ ID  
 NO:55, with Intron Y ORF3

<400> 58

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
 65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu

85										90					95				
Gln	Arg	Arg	Arg	Leu	Arg	Ala	Leu	Pro	Pro	Gln	Val	Ser	Cys	Leu	Lys				
			100					105					110						
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys				
		115					120					125							
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly				
	130					135					140								
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr				
145					150					155					160				
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg				
				165					170					175					
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu				
			180					185					190						
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro				
		195					200					205							
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala				
	210					215					220								
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser				
225					230					235					240				
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg				
				245					250					255					
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro				
			260					265					270						
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly				
		275					280					285							
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe				
	290					295					300								
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu				
305					310					315					320				
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln				
				325					330					335					
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp				
			340					345					350						
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser				
		355					360					365							
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu				
	370					375					380								
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu				

385                      390                      395                      400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
                                  405                      410                      415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
                                  420                      425                      430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
                                  435                      440                      445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
                                  450                      455                      460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
                                  465                      470                      475                      480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
                                  485                      490                      495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
                                  500                      505                      510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
                                  515                      520                      525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
                                  530                      535                      540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
                                  545                      550                      555                      560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
                                  565                      570                      575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
                                  580                      585                      590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
                                  595                      600                      605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
                                  610                      615                      620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
                                  625                      630                      635                      640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
                                  645                      650                      655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
                                  660                      665                      670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu  
                                  675                      680                      685  
 Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly



690

695

700

<210> 59  
 <211> 2645

<212> DNA

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); with Intron Y and Alpha

<400> 59

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atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcgggcg ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacggc cgcctccccc cgccccctcc ttccgccagg tgggcctccc cggggctcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgtgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccacaa 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgccctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgtgccact caggcccggc 660
ccccgcaca cgtagtga cccgaaggc gtctgggatg cgaacgggcc tggaaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc ggtgcgagg aggcgcgggg 780
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ttccc                                     2645

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<210> 60
<211> 841
<212> PRT
<213> Homo sapiens

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<220>
<223> Truncated Protein 2 (ver.2); encoded by SEQ ID
      NO:59, with Intron Y ORF1

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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
      35              40              45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
      50              55              60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
      65              70              75              80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
      85              90              95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
      100             105             110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
      115             120             125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
      130             135             140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
      145             150             155             160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
      165             170             175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
      180             185             190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
      195             200             205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
      210             215             220

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Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
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 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
 245 250 255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 260 265 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp  
 740 745 750  
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys  
 755 760 765  
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala  
 770 775 780  
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro  
 785 790 795 800  
 Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln  
 805 810 815  
 Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala  
 820 825 830

Gly Arg Ala Ala Pro Ala Phe Val Gly  
835 840

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<210> 61
<211> 756
<212> PRT
<213> Homo sapiens
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<220>  
<223> Truncated Protein 2 (ver.2); encoded by SEQ ID  
NO:59 with Intron Y ORF2 after the termination  
codon

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			20					25					30			
Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe	
		35					40					45				
Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Phe	
	50					55					60					
Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu	
65					70					75					80	
Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp	
				85					90					95		
Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala	
			100					105					110			
Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	Leu	Gly	
		115					120					125				
Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	Arg	Arg	
		130				135					140					
Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	Ala	Gly	
145					150					155					160	
Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	Gly	Ser	
				165					170					175		
Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala	
			180					185					190			
Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro	
		195					200					205				
Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	Val	Ser	Pro	
	210					215					220					

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460  
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
 530 535 540  
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
 545 550 555 560  
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
 595 600 605  
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
 610 615 620  
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
 625 630 635 640  
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
 645 650 655  
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp  
 660 665 670  
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr  
 675 680 685  
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val  
 690 695 700  
 Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro  
 705 710 715 720  
 Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg  
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 His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro  
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 Ala Phe Val Gly  
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<210> 62  
 <211> 841  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:  
 59 with Intron Y ORF3

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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg	35	40	45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro	50	55	60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg	65	70	75
Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu	85	90	95
Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys	100	105	110
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys	115	120	125
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly	130	135	140
Pro Pro Glu Ala Phe Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr	145	150	155
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg	165	170	175
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu	180	185	190
Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro	195	200	205
Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala	210	215	220
Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser	225	230	235
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg	245	250	255
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro	260	265	270
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly	275	280	285
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe	290	295	300
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu			



305                      310                      315                      320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
                                  325                                   330                                   335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
                                  340                                   345                                   350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
                                  355                                   360                                   365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
                                  370                                   375                                   380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
                                  385                                   390                                   395                                   400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
                                  405                                   410                                   415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
                                  420                                   425                                   430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
                                  435                                   440                                   445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
                                  450                                   455                                   460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
                                  465                                   470                                   475                                   480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
                                  485                                   490                                   495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
                                  500                                   505                                   510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
                                  515                                   520                                   525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
                                  530                                   535                                   540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
                                  545                                   550                                   555                                   560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
                                  565                                   570                                   575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
                                  580                                   585                                   590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
                                  595                                   600                                   605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg

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<210> 63
<211> 3500
<212> DNA
<213> Homo sapiens

<220>
<223> Reference Protein (ver.2); with Introns Y, Alpha
      and Beta

<400> 63
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gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
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<220>  
<223> Reference Protein (ver.2); with Introns Y, Alpha  
and Beta

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<400> 63
atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacggt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
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gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgggcctccc	cggggtcggc	240
gtccggctgg	ggttgagggc	ggccgggggg	aaccagcgac	atgcggagag	cagcgcaggc	300
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gggcccgcgg	gggccccccc	gaggccttca	ccaccagcgt	gcgcagctac	ctgcccacaa	480
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tccagtcca	gggatcccg	cagggctcca	tcctctccac	gctgctctgc	agcctgtgct	2640
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acttccctgt	agaagacgag	gccctgggtg	gcaaggcttt	tgttcagatg	ccggcccacg	2880
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actccagcta	tgcccggacc	tccatcagag	ccagtctcac	cttcaaccgc	ggcttcaagg	3000
ctggggaggaa	catgcgtcgc	aaactctttg	gggtcttgcg	gctgaagtgt	cacagcctgt	3060
ttctggattt	gcaggtgaac	agcctccaga	cgggtgtcac	caacatctac	aagatcctcc	3120
tgctgcaggc	gtacaggttt	cacgcagtgt	tgtcgcagct	cccatttcat	cagcaagttt	3180
ggaagaaccc	cacatttttc	ctgcgcgtca	tctctgacac	ggcctccctc	tgtactcca	3240
tctgaaagc	caagaacgca	gggatgtcgc	tggggggccaa	gggcgcggcc	ggccctctgc	3300
cctccgaggc	cgtgcagtg	ctgtgccacc	aagcattcct	gctcaagctg	actcgacacc	3360
gtgtcaccta	cgtgccactc	ctgggggtcac	tcaggacagc	ccagacgcag	ctgagtcgga	3420
agctcccggg	gacgacgctg	actgccctgg	aggccgcagc	caacccggca	ctgccctcag	3480
acttcaagac	catcctggag					3500

<210> 64  
 <211> 1165  
 <212> PRT  
 <213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63  
 with Intron Y ORF1

<400> 64

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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20           25           30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35           40           45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50           55           60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65           70           75           80
Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 85           90           95
Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
 100          105          110
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115          120          125
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 130          135          140
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 145          150          155          160
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 165          170          175
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
 180          185          190
Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
 195          200          205
Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 210          215          220
Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
 225          230          235          240
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg

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Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly				
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Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe				
	290					295					300								
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu				
305					310				315						320				
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln				
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His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp				
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Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser				
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Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu				
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Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu				
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Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu				
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Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly				
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Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro				
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Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys				
	450					455					460								
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg				
465					470				475					480					
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr				
				485				490						495					
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp				
		500						505					510						
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe				
		515					520					525							
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp				
	530					535					540								
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val				

545		550		555		560
Gly Cys Val Pro	Ala Ala Glu His Arg	Leu Arg Glu Glu Ile	Leu Ala			
	565	570	575			
Lys Phe Leu His	Trp Leu Met Ser Val Tyr Val Val	Glu Leu Leu Arg				
	580	585	590			
Ser Phe Phe Tyr	Val Thr Glu Thr Thr Phe Gln Lys	Asn Arg Leu Phe				
	595	600	605			
Phe Tyr Arg Lys	Ser Val Trp Ser Lys Leu Gln Ser	Ile Gly Ile Arg				
	610	615	620			
Gln His Leu Lys	Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu	Val				
	625	630	635			640
Arg Gln His Arg	Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg	Leu Arg				
	645	650	655			
Phe Ile Pro Lys	Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr					
	660	665	670			
Val Val Gly Ala	Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu					
	675	680	685			
Thr Ser Arg Val	Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala					
	690	695	700			
Arg Arg Pro Gly	Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile					
	705	710	715			720
His Arg Ala Trp	Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro					
	725	730	735			
Pro Pro Glu Leu	Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp					
	740	745	750			
Thr Ile Pro Gln	Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys					
	755	760	765			
Pro Gln Asn Thr	Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala					
	770	775	780			
Ala His Gly His	Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu					
	785	790	795			800
Thr Asp Leu Gln	Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu					
	805	810	815			
Thr Ser Pro Leu	Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu					
	820	825	830			
Asn Glu Ala Ser	Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys					
	835	840	845			
His His Ala Val	Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly					

850	855	860
Ile Pro Gln Gly Ser	Ile Leu Ser Thr	Leu Leu Cys Ser Leu Cys Tyr
865	870	875 880
Gly Asp Met Glu Asn Lys	Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu	
	885	890 895
Leu Leu Arg Leu Val Asp Asp Phe	Leu Leu Val Thr Pro His Leu Thr	
	900	905 910
His Ala Lys Thr Phe Leu Arg Thr	Leu Val Arg Gly Val Pro Glu Tyr	
	915	920 925
Gly Cys Val Val Asn Leu Arg Lys Thr	Val Val Asn Phe Pro Val Glu	
	930	935 940
Asp Glu Ala Leu Gly Gly Thr Ala Phe Val	Gln Met Pro Ala His Gly	
	945	950 955 960
Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val		
	965	970 975
Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu		
	980	985 990
Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu		
	995	1000 1005
Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln		
	1010	1015 1020
Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu		
	1025	1030 1035 1040
Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His		
	1045	1050 1055
Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp		
	1060	1065 1070
Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser		
	1075	1080 1085
Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln		
	1090	1095 1100
Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val		
	1105	1110 1115 1120
Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu		
	1125	1130 1135
Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala		
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Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp		

1155

1160

1165

<210> 65  
 <211> 1081  
 <212> PRT  
 <213> Homo sapiens

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<223> Reference Protein (ver.2); encoded by SEQ ID NO:63  
 with Intron Y ORF2 after the termination codon

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 Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
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 35 40 45  
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
 50 55 60  
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
 65 70 75 80  
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
 85 90 95  
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
 100 105 110  
 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
 115 120 125  
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
 130 135 140  
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
 145 150 155 160  
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
 165 170 175  
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240



Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460  
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525  
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
 545 550 555 560  
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
 595 600 605  
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
 610 615 620  
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
 625 630 635 640  
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
 645 650 655  
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp  
 660 665 670  
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr  
 675 680 685  
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val  
 690 695 700  
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro  
 705 710 715 720  
 Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg  
 725 730 735  
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser  
 740 745 750  
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg  
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 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser  
 770 775 780  
 Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn  
 785 790 795 800  
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val  
 805 810 815  
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe  
 820 825 830  
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn  
 835 840 845

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly  
 850 855 860  
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys  
 865 870 875 880  
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser  
 885 890 895  
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly  
 900 905 910  
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg  
 915 920 925  
 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln  
 930 935 940  
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg  
 945 950 955 960  
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys  
 965 970 975  
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys  
 980 985 990  
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys  
 995 1000 1005  
 Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His  
 1010 1015 1020  
 Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro  
 1025 1030 1035 1040  
 Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu  
 1045 1050 1055  
 Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu  
 1060 1065 1070  
 Pro Ser Asp Phe Lys Thr Ile Leu Asp  
 1075 1080

<210> 66  
 <211> 1165  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Reference Protein (ver.2); encoded by SEQ ID NO:63  
 with Intron Y ORF3

<400> 66

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 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
 65 70 75 80  
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu  
 85 90 95  
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys  
 100 105 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
 115 120 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 130 135 140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 145 150 155 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
 195 200 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
 210 215 220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
 225 230 235 240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
 245 250 255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 260 265 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp  
 740 745 750  
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys  
 755 760 765  
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala  
 770 775 780  
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu  
 785 790 795 800  
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu  
 805 810 815  
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu  
 820 825 830  
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys  
 835 840 845  
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly  
 850 855 860  
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr  
 865 870 875 880  
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu  
 885 890 895  
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr  
 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr  
           915                                  920                                  925  
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu  
           930                                  935                                  940  
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly  
   945                                  950                                  955                                  960  
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val  
                           965                                  970                                  975  
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu  
                           980                                  985                                  990  
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu  
                           995                                 1000                                 1005  
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln  
   1010                                 1015                                 1020  
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu  
  1025                                 1030                                 1035                                 1040  
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His  
                          1045                                 1050                                 1055  
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp  
                          1060                                 1065                                 1070  
 Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser  
                          1075                                 1080                                 1085  
 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln  
   1090                                 1095                                 1100  
 Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val  
  1105                                 1110                                 1115                                 1120  
 Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu  
                          1125                                 1130                                 1135  
 Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala  
                          1140                                 1145                                 1150  
 Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
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<210> 67  
 <211> 3173  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein (ver.2); with Introns Y, Alpha,  
       Beta and 2

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gtgctgccgc	tggccacgtt	cgtgcggcgc	ctggggcccc	agggctggcg	gctgggtgcag	120
cgcggggacc	cggcggtttt	ccgcgcgctg	gtggcccagt	gcctggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgggctctcc	cggggtcggc	240
gtccggttg	ggttgagggc	ggccgggggg	aaccagcgac	atgcggagag	cagcgcaggc	300
gactcagggc	gcttcccccg	caggtgtcct	gcctgaagga	gctggtggcc	cgagtgtctg	360
agaggctgtg	cgagcgcggc	gcgaagaacg	tgctggcctt	cggcttcgcg	ctgctggacg	420
gggcccgcg	gggccccccc	gaggccttca	ccaccagcgt	gcgcagctac	ctgcccaca	480
cggtgaccga	cgcactgcgg	gggagcgggg	cgtgggggct	gctgctgcgc	cgcgtgggcg	540
acgacgtgct	ggttcacctg	ctggcacgct	gcgcgctctt	tgtgctggtg	gctcccagct	600
gcgcctacca	ggtgtgcggg	ccgcccgtgt	accagctcgg	cgtgccact	caggccccgc	660
ccccgccaca	cgctagtggg	ccccgaaggc	gtctgggatg	cgaacgggcc	tggaaccata	720
gcgtcagggg	ggccgggggtc	cccctggggc	tgccagcccc	gggtgcgagg	aggcgcgggg	780
gcagtgccag	ccgaagtctg	ccgttgccca	agaggccag	gcgtggcgct	gccccgagc	840
cggagcggac	gcccgttggtg	caggggtcct	gggcccaccc	gggcaggacg	cgtggaccga	900
gtgaccgtgg	tttctgtgtg	gtgtcacctg	ccagaccgcg	cgaagaagcc	acctcttttg	960
aggggtgcgt	ctctggcacg	cgccactccc	acccatccgt	gggcccgcag	caccacgcgg	1020
gccccccatc	cacatcgcg	ccaccacgtc	cctgggacac	gccttgtccc	ccgtgttacg	1080
ccgagaccaa	gcacttccc	tactcctcag	gcgacaagga	gcagctgcgg	ccctccttcc	1140
tactcagctc	tctgaggccc	agcctgactg	gcgctcggag	gctcgtggag	accatctttc	1200
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actggcaaat	gcggccccctg	tttctggagc	tgcttgggaa	ccacgcgcag	tgccccctacg	1320
gggtgctcct	caagacgcac	tgcccgtctg	gagctgcggt	caccccagca	gccggtgtct	1380
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gcttctcag	gaacaccaag	aagttcatct	ccctggggaa	gcattgcaag	ctctcgtctg	1620
aggagctgac	gtggaagatg	agcgtgcggg	actgcgctg	gctgcgcagg	agcccagggg	1680
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actggctgat	gagtgtgtac	gtcgtcgagc	tgctcaggtc	tttcttttat	gtcacggaga	1800
ccacgtttca	aaagaacagg	ctctttttct	accggaagag	tgtctggagc	aagttgcaaa	1860
gcatttgaat	cagacagcac	ttgaagaggg	tgacgtgcg	ggagctgtcg	gaagcagagg	1920
tcaggcagca	tcgggaagcc	aggcccgcgc	tgctgacgtc	cagactccgc	ttcatcccca	1980
agcctgacgg	gctgcggccg	attgtgaaca	tggactacgt	cgtgggagcc	agaacgttcc	2040
gcagagaaaa	gagggccgag	cgtctcacct	cgagggtgaa	ggcactgttc	agcgtgctca	2100
actacgagcg	ggcgcggcgc	cccggcctcc	tgggcgcctc	tgtgctgggc	ctggacgata	2160
tccacagggc	ctggcgcaac	ttcgtgctgc	gtgtgcgggc	ccaggacccg	ccgcctgagc	2220
tgtactttgt	caaggtggat	gtgacgggcg	cgtacgacac	catccccag	gacaggctca	2280
cggaggtcat	cgccagcatc	atcaaaccct	agaacacgta	ctgcgtgcgt	cggtatgccg	2340
tgggtccagaa	ggccgcccac	gggcacgtcc	gcaaggcctt	caagagccac	gtctctacct	2400
tgacagacct	ccagccgtac	atgcgacagt	tcgtggtctc	cctgcaggag	accagcccgc	2460
tgagggatgc	cgtcgtcatc	gagcagagct	cctccctgaa	tgaggccagc	agtggcctct	2520
tcgacgtctt	cctacgcttc	atgtgccacc	acgcctgctg	catcaggggc	aagtcctacg	2580
tccagtgcc	gggatcccg	cagggtccca	tcctctccac	gctgctctgc	agcctgtgct	2640
acggcgacat	ggagaacaag	ctgtttgcgg	ggattcggcg	ggacgggctg	ctcctgcgtt	2700
tgggtgatga	tttcttggtg	gtgacacctc	acctcaccca	cgcgaaaacc	ttcctcagga	2760
ccctggtccg	aggtgtccct	gagtatggct	gcgtgggtgaa	cttgcggaag	acagtgtgta	2820
acttccctgt	agaagacgag	gccctgggtg	gcacggcttt	tggtcagatg	ccggccccacg	2880
gcctattccc	ctggtgcggc	ctgctgctgg	ataccgggac	cctggaggtg	cagagcgact	2940
actccaggtg	agcgcacctg	gcccgaagtg	gagcctgtgc	ccggctgggg	caggtgctgc	3000
tgcagggccg	ttgcgtccac	ctctgcttcc	gtgtggggca	ggcgactgcc	aatcccaaa	3060
ggtcagatgc	cacaggggtg	ccctcgtccc	atctggggct	gagcacaat	gcattctttct	3120
gtgggagtga	gggtgcctca	caacggggagc	agttttctgt	gctatttttg	ttaa	3173

&lt;210&gt; 68



<211> 982  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 3 (ver.2); encoded by SEQ ID  
 NO:67 with Intron Y ORF1

<400> 68

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His	Thr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	20	25	30	
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	35	40	45	
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	50	55	60	
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Gly	Leu	Pro	Gly	Val	Gly	65	70	75	80
Val	Arg	Leu	Gly	Leu	Arg	Ala	Ala	Gly	Gly	Asn	Gln	Arg	His	Ala	Glu	85	90	95	
Ser	Ser	Ala	Gly	Asp	Ser	Gly	Arg	Phe	Pro	Arg	Arg	Ser	Cys	Leu	Lys	100	105	110	
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	115	120	125	
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	130	135	140	
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	145	150	155	160
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	165	170	175	
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	180	185	190	
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	195	200	205	
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	210	215	220	
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	225	230	235	240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	245	250	255	

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 260 265 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560

Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	
				565					570					575		
Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	
				580					585					590		
Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	
				595					600					605		
Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	
				610					615					620		
Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	
				625					630					635		
Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	
				645					650					655		
Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	
				660					665					670		
Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	
				675					680					685		
Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	
				690					695					700		
Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	
				705					710					715		
His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	
				725					730					735		
Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	
				740					745					750		
Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	
				755					760					765		
Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	
				770					775					780		
Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	
				785					790					795		
Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	
				805					810					815		
Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	
				820					825					830		
Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	
				835					840					845		
His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	
				850					855					860		

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr  
 865 870 875 880  
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu  
 885 890 895  
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr  
 900 905 910  
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr  
 915 920 925  
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu  
 930 935 940  
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly  
 945 950 955 960  
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val  
 965 970 975  
 Gln Ser Asp Tyr Ser Arg  
 980

<210> 69  
 <211> 897  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 3 (ver.2); encoded by SEQ ID  
 NO:67 with Intron Y ORF2 after the termination  
 codon

<400> 69  
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 Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
 20 25 30  
 Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
 35 40 45  
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
 50 55 60  
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
 65 70 75 80  
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
 85 90 95  
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
 115 120 125  
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
 130 135 140  
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
 145 150 155 160  
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
 165 170 175  
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460  
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525  
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
 530 535 540  
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
 545 550 555 560  
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
 595 600 605  
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
 610 615 620  
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
 625 630 635 640  
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
 645 650 655  
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp  
 660 665 670  
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr  
 675 680 685  
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val  
 690 695 700  
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro  
 705 710 715 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg  
                               725                              730                              735  
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser  
                               740                              745                              750  
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg  
                               755                              760                              765  
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser  
                               770                              775                              780  
 Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn  
                               785                              790                              795                              800  
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val  
                               805                              810                              815  
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe  
                               820                              825                              830  
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn  
                               835                              840                              845  
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly  
                               850                              855                              860  
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys  
                               865                              870                              875                              880  
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser  
                               885                              890                              895

Arg

<210> 70

<211> 982

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3 (Ver.2); encoded by SEQ ID  
NO:67 with Intron Y ORF3

<400> 70

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20                              25                              30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35                              40                              45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

50					55					60					
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Pro	Pro	Arg	Gly	Arg	Arg
65					70					75					80
Pro	Ala	Gly	Val	Glu	Gly	Gly	Arg	Gly	Glu	Pro	Ala	Thr	Cys	Gly	Glu
				85					90					95	
Gln	Arg	Arg	Arg	Leu	Arg	Ala	Leu	Pro	Pro	Gln	Val	Ser	Cys	Leu	Lys
				100				105					110		
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys
		115					120					125			
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly
		130				135					140				
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr
						150					155				160
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg
				165					170					175	
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu
			180					185					190		
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro
		195					200					205			
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
		210					215				220				
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
				225			230				235				240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
				245					250					255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
				260				265					270		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
				275			280					285			
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe
				290			295					300			
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu
				305			310				315				320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
				325					330					335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
				340				345					350		
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser



355	360	365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu		
370	375	380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu		
385	390	395
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu		
405	410	415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly		
420	425	430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro		
435	440	445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys		
450	455	460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg		
465	470	475
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr		
485	490	495
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp		
500	505	510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe		
515	520	525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp		
530	535	540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val		
545	550	555
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala		
565	570	575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg		
580	585	590
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe		
595	600	605
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg		
610	615	620
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val		
625	630	635
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg		
645	650	655
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr		

660					665					670					
Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu
		675					680					685			
Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala
	690					695					700				
Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile
705				710						715					720
His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro
				725					730					735	
Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp
			740					745						750	
Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys
		755					760					765			
Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala
	770					775					780				
Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu
785				790					795						800
Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu
				805					810					815	
Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu
			820					825					830		
Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys
		835					840					845			
His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly
	850					855					860				
Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr
865						870					875				880
Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu
				885					890					895	
Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr
			900					905					910		
His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr
		915					920					925			
Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu
	930					935					940				
Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly
945				950						955					960
Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val

965

970

975

Gln Ser Asp Tyr Ser Arg  
980

<210> 71  
<211> 3466  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Altered C-Terminus Protein (ver.2); with Introns  
Y, Alpha, Beta and 3

<400> 71  
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cgcggggacc cgcgcgcttt ccgcgcgcgt gtggcccagt gcctgggtgt cgtgccctgg 180  
gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240  
gtccggctgg gggttagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300  
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtgc 360  
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggttcgcg ctgctggacg 420  
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgccaaca 480  
cggtgaccga cgcactgcgg ggagcgggg cgtaggggct gctgctgcgc cgctggggcg 540  
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600  
gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgctgccact caggcccggc 660  
ccccgccaca cgctagtggg ccccgaaagg gtctgggatg cgaacggggc tggaaccata 720  
gcgtcagggg ggccggggtc cccctgggcc tgccagcccc ggggtgcgag aggcgcgggg 780  
gcagtgccag ccgaagtctg ccgttgccca agaggccag gcgtggcgct gccctgagc 840  
cggagcggac gcccgttggg caggggtcct gggccacccc gggcaggacg cgtggaccga 900  
gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc acctcttgg 960  
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020  
gcccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080  
ccgagaccaa gcacttcttc tactctcag gcgacaagga gcagctgcgg cctctcttc 1140  
tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatcttc 1200  
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gtgcccggga gaagccccag ggctctgtgg cgcccccca ggaggaggac acagacccc 1440  
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gggcctgcct gcgccggtg gtgccccag gccctctggg ctccaggcac aacgaacgcc 1560  
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ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860  
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920  
tcaggcagca tcgggaagcc aggccccccc tgctgacgtc cagactccgc ttcaccccc 1980  
agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040  
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actacgagcg ggcgcgcgcc cccggcctcc tgggcgctc tgtgctgggc ctggacgata 2160  
tccacagggc ctggcgccac ttctgtctgc gtgtgcgggc ccaggacccg ccgctgagc 2220  
tgtactttgt caaggtggat gtgacgggcg cgtacgacac catccccag gacaggtca 2280  
cggaggtcat cgccagcatc atcaaaccac agaacacgta ctgcgtgcgt cggtatgccg 2340  
tgggtccagaa ggccgcccac gggcacgtcc gcaaggcctt caagagccac gtctctacct 2400  
tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag accagcccg 2460

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tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc agtggcctct 2520
tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc aagtcctacg 2580
tccagtgccg ggggatcccg cagggctcca tcctctccac gctgctctgc agcctgtgct 2640
acggcgacat ggagaacaag ctgtttgogg ggattcggcg ggacgggctg ctctgcgtt 2700
tgggtgatga tttctgttg gtgacacctc acctcaccca cgcgaaaacc ttctcagga 2760
ccctgggccg aggtgtccct gagtatggct gcgtggtgaa cttgcggaag acagtgggta 2820
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gcctattccc ctggtgcggc ctgctgctgg ataccggac cctggagggtg cagagcgact 2940
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ttctggattt gcaggtgaac agcctccaga cgggtgtgcac caacatctac aagatcctcc 3120
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tcctgaaagc caagaacgca gccgaagaaa acatttctgt cgtgactcct gcggtgcttg 3300
ggctcgggaca gccagagatg gagccacccc gcagaccgtc ggggtgtgggc agctttcccg 3360
tgtctcctgg gaggggagtt gggctgggcc tgtgactcct cagcctctgt tttccccag 3420
ggatgtcgct gggggccaag ggcgcgcgcg gccctctgcc ctccga 3466

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<210> 72  
 <211> 1130  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Altered C-Terminus Protein (ver.2); encoded by SEQ  
 ID NO:71 with Intron Y ORF1

<400> 72  
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
     1                    5                    10                    15  
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
             20                    25                    30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
             35                    40                    45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
             50                    55                    60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
             65                    70                    75                    80  
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
             85                    90                    95  
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
             100                    105                    110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
             115                    120                    125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
             130                    135                    140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
             145                    150                    155                    160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
 195 200 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
 210 215 220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
 225 230 235 240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
 245 250 255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 260 265 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp  
 740 745 750  
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys  
 755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala  
 770 775 780  
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu  
 785 790 795 800  
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu  
 805 810 815  
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu  
 820 825 830  
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys  
 835 840 845  
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly  
 850 855 860  
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr  
 865 870 875 880  
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu  
 885 890 895  
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr  
 900 905 910  
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr  
 915 920 925  
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu  
 930 935 940  
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly  
 945 950 955 960  
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val  
 965 970 975  
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu  
 980 985 990  
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu  
 995 1000 1005  
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln  
 1010 1015 1020  
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu  
 1025 1030 1035 1040  
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His  
 1045 1050 1055  
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp  
 1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu  
 1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro  
 1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val  
 1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
 1125 1130

<210> 73

<211> 1045

<212> PRT

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ  
 ID NO:71 with Intron Y ORF2 after the termination  
 codon

<400> 73

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr  
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
 165 170 175



Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460  
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525  
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
 530 535 540  
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
 545 550 555 560  
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
 595 600 605  
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
 610 615 620  
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
 625 630 635 640  
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
 645 650 655  
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp  
 660 665 670  
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr  
 675 680 685  
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val  
 690 695 700  
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro  
 705 710 715 720  
 Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg  
 725 730 735  
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser  
 740 745 750  
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg  
 755 760 765  
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser  
 770 775 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn  
 785 790 795 800  
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val  
 805 810 815  
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe  
 820 825 830  
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn  
 835 840 845  
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly  
 850 855 860  
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys  
 865 870 875 880  
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser  
 885 890 895  
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly  
 900 905 910  
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg  
 915 920 925  
 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln  
 930 935 940  
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg  
 945 950 955 960  
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys  
 965 970 975  
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys  
 980 985 990  
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn Ile Leu Val  
 995 1000 1005  
 Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met Glu Pro Pro  
 1010 1015 1020  
 Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro Gly Arg Gly  
 1025 1030 1035 1040  
 Val Gly Leu Gly Leu  
 1045

&lt;210&gt; 74

&lt;211&gt; 1130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ  
ID NO:71 with Intron Y ORF3

&lt;400&gt; 74

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu  
85 90 95

Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys  
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
210 215 220

Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
245 250 255

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
260 265 270

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp  
 740 745 750  
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys  
 755 760 765  
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala  
 770 775 780  
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu  
 785 790 795 800  
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu  
 805 810 815  
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu  
 820 825 830  
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys  
 835 840 845  
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly  
 850 855 860  
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr  
 865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu  
                             885                            890                            895  
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr  
                             900                            905                            910  
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr  
                             915                            920                            925  
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu  
                             930                            935                            940  
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly  
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 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val  
                             965                            970  975  
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu  
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 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu  
                             995                            1000                            1005  
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln  
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 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu  
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 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His  
                             1045                            1050                            1055  
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp  
                             1060                            1065                            1070  
 Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu  
                             1075                            1080                            1085  
 Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro  
                             1090                            1095                            1100  
 Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val  
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 Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
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&lt;210&gt; 75

&lt;211&gt; 4022

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

 <223> Protein Lacking Motif A (ver.2); with Introns Y  
 and Beta

&lt;400&gt; 75

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gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgggcctccc	cggggtcggc	240
gtccggctgg	ggttaggggc	ggccgggggg	aaccagcgac	atgcggagag	cagcgaggc	300
gactcagggc	gcttcccccg	caggtgtcct	gcctgaagga	gctggtggcc	cgagtgtctg	360
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cggtgaccga	cgcaactgcg	gggagcgggg	cgtgggggct	gctgctgcgc	cgctggggcg	540
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gcgcctacca	ggtgtgcggg	ccgcgcgctg	accagctcgg	cgctgccact	caggccccgg	660
ccccgccaca	cgctagtggg	ccccgaaggc	gtctgggatg	cgaacggggc	tggaaaccata	720
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gcagtgccag	ccgaagtctg	ccgttgccca	agaggcccag	gcgtggcgct	gcccctgagc	840
cggagcggac	gcccgttggg	caggggtcct	gggccacccc	gggcaggacg	cgtggaccga	900
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agcctgacgg	gctgcggccg	attgtgaaca	tggactacgt	cgtgggagcc	agaacgttcc	2040
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ccaagggcgc	cgccggccct	ctgccctccg	aggccgtgca	gtggctgtgc	caccaagcat	3300



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tcctgctcaa gctgactcga caccgtgtca cctacgtgcc actcctgggg tcactcagga 3360
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cagccaaccc ggcaactgccc tcagacttca agaccatcct ggactgatgg ccaccgcgcc 3480
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gaccaaaggt gtgccctgta cacaggcgag gaccctgcac ctggatgggg gtccctgtgg 3960
gtcaaatggg ggggaggtgc tgtgggagta aaatactgaa tatatgagtt tttcagtttt 4020
ga

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<210> 76

<211> 1154

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID  
NO:75 with Intron Y ORF1

<400> 76

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
      20              25              30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
      35              40              45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
      50              55              60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
      65              70              75              80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
      85              90              95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
      100              105              110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
      115              120              125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
      130              135              140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
      145              150              155              160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
      165              170              175

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Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
 195 200 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
 210 215 220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
 225 230 235 240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
 245 250 255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 260 265 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala  
 740 745 750  
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val  
 755 760 765  
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His  
 770 775 780

Val	Ser	Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	785	790	795	800
His	Leu	Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	805	810	815	
Ser	Ser	Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	820	825	830	
Arg	Phe	Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	835	840	845	
Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	850	855	860	
Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	865	870	875	880
Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	885	890	895	
Pro	His	Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	900	905	910	
Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	915	920	925	
Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	930	935	940	
Pro	Ala	His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	945	950	955	960
Thr	Leu	Glu	Val	Gln	Ser	Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	965	970	975	
Arg	Ala	Ser	Leu	Thr	Phe	Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	980	985	990	
Arg	Arg	Lys	Leu	Phe	Gly	Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	995	1000	1005	
Leu	Asp	Leu	Gln	Val	Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	1010	1015	1020	
Lys	Ile	Leu	Leu	Leu	Gln	Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	1025	1030	1035	1040
Leu	Pro	Phe	His	Gln	Gln	Val	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	1045	1050	1055	
Val	Ile	Ser	Asp	Thr	Ala	Ser	Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	1060	1065	1070	
Asn	Ala	Gly	Met	Ser	Leu	Gly	Ala	Lys	Gly	Ala	Ala	Gly	Pro	Leu	Pro	1075	1080	1085	

Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu  
 1090 1095 1100

Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr  
 1105 1110 1115 1120

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala  
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Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile  
 1140 1145 1150

Leu Asp

<210> 77  
 <211> 1069  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Protein Lacking Motif A (ver.2); encoded by SEQ ID  
 NO:75 with Intron Y ORF2 after the termination  
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 35 40 45  
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
 50 55 60  
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
 65 70 75 80  
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
 85 90 95  
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
 100 105 110  
 Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
 115 120 125  
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
 130 135 140  
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
 165 170 175  
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
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Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525  
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
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 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
 545 550 555 560  
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
 595 600 605  
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
 610 615 620  
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
 625 630 635 640  
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
 645 650 655  
 Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro  
 660 665 670  
 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala  
 675 680 685  
 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr  
 690 695 700  
 Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr  
 705 710 715 720  
 Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn  
 725 730 735  
 Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His  
 740 745 750  
 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile  
 755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly  
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 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu  
 785 790 795 800  
 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His  
 805 810 815  
 Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly  
 820 825 830  
 Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp  
 835 840 845  
 Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu  
 850 855 860  
 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln  
 865 870 875 880  
 Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr  
 885 890 895  
 Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe  
 900 905 910  
 Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val  
 915 920 925  
 Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu  
 930 935 940  
 Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln  
 945 950 955 960  
 Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr  
 965 970 975  
 Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser  
 980 985 990  
 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln  
 995 1000 1005  
 Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val  
 1010 1015 1020  
 Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu  
 1025 1030 1035 1040  
 Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala  
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 Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
 1060 1065



<210> 78  
 <211> 1154  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Protein Lacking Motif A (ver.2); encoded by SEQ ID  
 NO:75 with Intron Y ORF3

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           20                  25                  30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
           35                  40                  45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
   50                  55                  60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
   65                  70                  75                  80  
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu  
           85                  90                  95  
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys  
           100                  105                  110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
   115                  120                  125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
   130                  135                  140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
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 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
           165                  170                  175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
           180                  185                  190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
   195                  200                  205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
   210                  215                  220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
   225                  230                  235                  240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg

				245				250				255				
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	
				260					265					270		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	
				275					280					285		
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	
				290					295					300		
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	
				305					310					315		
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	
				325					330					335		
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	
				340					345					350		
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	
				355					360					365		
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	
				370					375					380		
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	
				385					390					395		
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	
				405					410					415		
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	
				420					425					430		
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	
				435					440					445		
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	
				450					455					460		
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	
				465					470					475		
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	
				485					490					495		
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	
				500					505					510		
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	
				515					520					525		
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	
				530					535					540		
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	

545					550					555				560	
Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala
				565					570					575	
Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg
			580					585					590		
Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe
		595					600					605			
Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg
	610					615					620				
Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val
625					630					635					640
Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg
				645					650					655	
Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr
			660					665					670		
Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu
		675					680					685			
Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala
	690					695					700				
Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile
705					710					715					720
His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro
				725					730					735	
Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala
			740					745					750		
Ser	Ile	Ile	Lys	Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val
		755					760					765			
Val	Gln	Lys	Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His
	770					775					780				
Val	Ser	Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala
785					790					795					800
His	Leu	Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln
				805					810					815	
Ser	Ser	Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu
			820					825					830		
Arg	Phe	Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val
		835					840					845			

850	855	860
Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg 865 870 875 880		
Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr 885 890 895		
Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly 900 905 910		
Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn 915 920 925		
Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met 930 935 940		
Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg 945 950 955 960		
Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile 965 970 975		
Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met 980 985 990		
Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe 995 1000 1005		
Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr 1010 1015 1020		
Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln 1025 1030 1035 1040		
Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg 1045 1050 1055		
Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys 1060 1065 1070		
Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro 1075 1080 1085		
Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu 1090 1095 1100		
Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr 1105 1110 1115 1120		
Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala 1125 1130 1135		
Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile 1140 1145 1150		
Leu Asp		

<210> 79  
 <211> 3137  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein Lacking Motif A (ver.2); with  
 Introns Y, Beta and 2

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 cgccggggacc cggcggtttt ccgcgcgtg gtggccaggt gcctgggtgtg cgtgccctgg 180  
 gacgcacggc cggccccgcg cggccccctc ttccgccagg tgggcctccc cgggggtcggc 240  
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 agaggctgtg cgagcgcggc gcgaagaacg tgetggcctt cggcttcgcg ctgctggacg 420  
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tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
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ggcaggcgac tgccaatccc aaagggtcag atgccacagg gtgcccctcg tcccatctgg 3060
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<210> 80  
 <211> 970  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein lacking Motif A (ver.2); encoded  
 by SEQ ID NO:79 with Intron Y ORF1

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 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
 65 70 75 80  
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
 85 90 95  
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
 100 105 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
 115 120 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 130 135 140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 145 150 155 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
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 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro

195					200					205					
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
210						215					220				
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
225					230					235					240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
				245					250					255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
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Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
			275				280					285			
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe
290					295					300					
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu
305					310					315					320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
				325					330					335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
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Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser
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Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu
370					375					380					
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu
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Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu
				405					410					415	
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly
			420					425					430		
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro
		435					440					445			
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys
		450				455					460				
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg
465					470					475					480
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr
				485					490					495	
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp

500	505	510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 515 520 525		
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530 535 540		
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 545 550 555 560		
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 570 575		
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 580 585 590		
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 595 600 605		
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg 610 615 620		
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 625 630 635 640		
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 645 650 655		
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 660 665 670		
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu 675 680 685		
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 690 695 700		
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 705 710 715 720		
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro 725 730 735		
Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala 740 745 750		
Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val 755 760 765		
Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His 770 775 780		
Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala 785 790 795 800		
His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln		





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<400> 81
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr
  1          5          10          15
Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
          20          25          30
Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe
          35          40          45
Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe
          50          55          60
Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu

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65		70		75		80
Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp						
	85			90		95
Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala						
	100			105		110
Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly						
	115			120		125
Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg						
	130			135		140
Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly						
	145			150		155
Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser						
				165		170
Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala						
	180			185		190
Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro						
	195			200		205
Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro						
	210			215		220
Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly						
	225			230		235
Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro						
				245		250
Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro						
	260			265		270
Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu						
	275			280		285
Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr						
	290			295		300
Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp						
	305			310		315
Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp						
				325		330
Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys						
	340			345		350
Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val						
	355			360		365
Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val						

370                      375                      380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385                      390                      395                      400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
                     405                      410                      415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
                     420                      425                      430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
                     435                      440                      445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
                     450                      455                      460  
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465                      470                      475                      480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
                     485                      490                      495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
                     500                      505                      510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
                     515                      520                      525  
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
                     530                      535                      540  
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
 545                      550                      555                      560  
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
                     565                      570                      575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
                     580                      585                      590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
                     595                      600                      605  
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
                     610                      615                      620  
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
 625                      630                      635                      640  
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
                     645                      650                      655  
 Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro  
                     660                      665                      670  
 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala

675                      680                      685  
 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr  
     690                      700  
 Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr  
     705                      710                      715                      720  
 Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn  
                     725                      730                      735  
 Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His  
                     740                      745                      750  
 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile  
                     755                      760                      765  
 Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly  
                     770                      775                      780  
 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu  
     785                      790                      795                      800  
 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His  
                     805                      810                      815  
 Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly  
                     820                      825                      830  
 Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp  
                     835                      840                      845  
 Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu  
                     850                      855                      860  
 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln  
     865                      870                      875                      880  
 Ser Asp Tyr Ser Arg  
                     885

<210> 82  
 <211> 970  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein lacking Motif A (ver.2); encoded  
 by SEQ ID NO:79 with Intron Y ORF3

<400> 82  
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
     1                      5                      10                      15  
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
                     20                      25                      30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
 65 70 75 80  
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu  
 85 90 95  
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys  
 100 105 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
 115 120 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 130 135 140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 145 150 155 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
 195 200 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
 210 215 220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
 225 230 235 240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
 245 250 255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 260 265 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala  
 740 745 750  
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val  
 755 760 765  
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His  
 770 775 780  
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala  
 785 790 795 800  
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln  
 805 810 815  
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu  
 820 825 830  
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val  
 835 840 845  
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys  
 850 855 860  
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg  
 865 870 875 880  
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr  
 885 890 895  
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly  
 900 905 910  
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn  
 915 920 925  
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met  
 930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg  
 945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg  
 965 970

<210> 83  
 <211> 3432  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Protein Lacking Motif A and Altered C-Terminus  
 (ver.2); with Intron Y, Beta and 3

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 cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180  
 gacgcacggc cgcggggcgc cgcggcctcc ttccgccagg tgggcctccc cggggtcggc 240  
 gtccggctgg ggttaggggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300  
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgtgc 360  
 agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420  
 gggcccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgccaaca 480  
 cggtagccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540  
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600  
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 ccccgccaca cgctagtggg cccgaaggc gtctgggatg cgaacgggccc tggaccata 720  
 gcgtcaggga ggccggggtc cccctgggccc tgccagcccc ggggtgcgagg aggcgcgggg 780  
 gcagtgccag ccgaagtctg ccgttgccca agaggcccg cgtggcgct gcccctgagc 840  
 cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900  
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960  
 agggctgcgt ctctggcacg cgcactccc acccatccgt gggccgccag caccacgcgg 1020  
 gcccccacac cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080  
 ccgagaccaa gcaattcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140  
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatcttcc 1200  
 tgggttccag gccctggatg ccagggactc cccgcagggt gccccgcctg cccagcgt 1260  
 actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320  
 ggggtgctcct caagacgcac tgcccgtgc gaagctgcgt caccacagca gccggtgtct 1380  
 gtgcccggga gaagccccag ggctctgtgg cggcccccca ggaggaggac acagaccccc 1440  
 gtgcctggt gcagctgctc cgcagcaca gcagccccg gcaggtgtac ggcttcgtgc 1500  
 gggcctgcct gcgcggctg gtgccccag gccctgggg ctccaggcac aacgaacgcc 1560  
 gcttctcag gaacaccaag aagttcatct ccctgggaa gcatgccaa ctctcgtgc 1620  
 aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680  
 ttggctgtgt tccggccgca gagcaccgtc tgctgagga gatcctggcc aagttcctgc 1740  
 actggctgat gagtgtgtac gtctcagac tgctcaggtc tttcttttat gtcacggaga 1800  
 ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860  
 gcattggaat cagacagcac ttgaagaggg tgacgtgcg ggagctgtcg gaagcagagg 1920  
 tcaggcagca tcgggaagcc agggccgccc tgctgacgtc cagactccgc ttcaccccca 1980  
 agcctgacgg gctgcggcgc attgtgaaca tggactacgt cgtgggagcc agaacttcc 2040  
 gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgtca 2100  
 actacgagcg ggcgcggcgc cccggcctcc tgggcgctc tgtgctgggc ctggacgata 2160  
 tccacagggc ctgggcgacc ttctgtgtgc gtgtgcgggc ccaggacccg ccgctgagc 2220  
 tgtactttgt caaggacagg ctacaggagg tcatcgccag catcatcaaa cccagaaca 2280  
 cgtactgcgt gcgtcggtat gccgtggtcc agaaggccgc ccatgggcac gtccgcaagg 2340



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ccttcaagag ccacgtctct accttgacag acctccagcc gtacatgcga cagttcgtgg 2400
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ccacgctgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640
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cccacgcgaa aaccttcctc aggaccctgg tccgaggtgt ccctgagtat ggctgcgtgg 2760
tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
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ggaccctgga ggtgcagagc gactactcca gctatgcccg gacctccatc agagccagtc 2940
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agctccatt tcatacagaa gtttggaaga accccacatt tttcctgcgc gtcactctctg 3180
acacggcctc cctctgctac tccatcctga aagccaagaa cgcagccgaa gaaaacattt 3240
ctgtcgtgac tctgcgggtg cttgggtcgg gacagccaga gatggagcca cccgcagac 3300
cgtcgggtgt gggcagcttt ccggtgtctc ctgggagggg agttgggctg ggctgtgac 3360
tctcagcct ctgttttccc ccagggatgt cgctgggggc caagggcgcc gccggccctc 3420
tgccctccga ga 3432

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<210> 84  
 <211> 1122  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Protein Lacking Motif A and Altered C-Terminus  
 (ver.2); encoded by SEQ ID NO:83 with Intron Y  
 ORF1

<400> 84  
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser.  
     1                    5                    10                    15  
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
             20                    25                    30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
             35                    40                    45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
             50                    55                    60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
             65                    70                    75                    80  
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
                     85                    90                    95  
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
             100                    105                    110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
             115                    120                    125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
             130                    135                    140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 145 150 155 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
 195 200 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
 210 215 220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
 225 230 235 240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
 245 250 255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 260 265 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala  
 740 745 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val  
 755 760 765  
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His  
 770 775 780  
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala  
 785 790 795 800  
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln  
 805 810 815  
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu  
 820 825 830  
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val  
 835 840 845  
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys  
 850 855 860  
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg  
 865 870 875 880  
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr  
 885 890 895  
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly  
 900 905 910  
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn  
 915 920 925  
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met  
 930 935 940  
 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg  
 945 950 955 960  
 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile  
 965 970 975  
 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met  
 980 985 990  
 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe  
 995 1000 1005  
 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr  
 1010 1015 1020  
 Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln  
 1025 1030 1035 1040  
 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg  
 1045 1050 1055

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys  
                   1060                  1065                  1070

Asn Ala Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly  
                   1075                  1080                  1085

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly  
                   1090                  1095                  1100

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile  
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Gly Ala

<210> 85  
 <211> 1037  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Protein Lacking Motif A and Altered C-Terminus  
       (ver.2); encoded by SEQ ID NO:83 with Intron Y  
       ORF2 after the termination codon

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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
                   20                  25                  30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
                   35                  40                  45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
                   50                  55                  60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
   65                  70                  75                  80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
                   85                  90                  95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
                   100                  105                  110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
                   115                  120                  125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
                   130                  135                  140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
                   145                  150                  155                  160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
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 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
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 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
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 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
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 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
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 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
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 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
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 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
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 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
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 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
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 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
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 Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro  
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 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala  
 675 680 685  
 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr  
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 Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr  
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 Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn  
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 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile  
 755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly  
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 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu  
 785 790 795 800  
 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His  
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 Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly  
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 Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp  
 835 840 845  
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 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln  
 865 870 875 880  
 Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr  
 885 890 895  
 Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe  
 900 905 910  
 Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val  
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 Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu  
 930 935 940  
 Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln  
 945 950 955 960  
 Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr  
 965 970 975  
 Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu  
 980 985 990  
 Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu  
 995 1000 1005  
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 Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile Gly Ala  
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&lt;210&gt; 86

&lt;211&gt; 1122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens



&lt;220&gt;

<223> Protein Lacking Motif A and Altered C-Terminus  
(ver.2); encoded by SEQ ID NO:83 with Intron Y  
ORF3

&lt;400&gt; 86

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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
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Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
      50           55           60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
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Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
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Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
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Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
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Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
      130          135          140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
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Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
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Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
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Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
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Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
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Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser
      225          230          235          240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
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Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
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 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
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 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
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 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
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 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
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Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
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 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
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 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
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 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
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 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
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 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala  
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 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val  
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 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His  
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 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala  
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 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln  
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 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val  
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 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys  
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Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr  
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&lt;210&gt; 87

&lt;211&gt; 7615

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; Human Telomerase Clone with Exon Beta Spliced Out

&lt;400&gt; 87

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<212> PRT
<213> Homo sapiens

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<400> 90
Ala Val Arg Ile Arg Gly Lys Ser
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<210> 91
<211> 8
<212> PRT
<213> Unknown

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<223> Description of Unknown Organism: Consensus P-loop
      Motif Sequence found in large number of protein
      families

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<220>
<221> MOD_RES
<222> (2)..(5)
<223> Wherein Xaa is any residue

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<400> 91
Ala Xaa Xaa Xaa Xaa Gly Lys Ser
  1                      5

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<210> 92
<211> 17
<212> PRT
<213> Homo sapiens

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<400> 92
Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Cys Val
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Gly

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<210> 93
<211> 9
<212> PRT
<213> Unknown

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&lt;220&gt;

<223> Description of Unknown Organism: Consensus c-Alb  
SH3 binding peptide

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (2)..(5)

&lt;223&gt; Wherein Xaa is any residue

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (7)..(8)

&lt;223&gt; Wherein Xaa is any residue

&lt;400&gt; 93

Pro Xaa Xaa Xaa Xaa Pro Xaa Xaa Pro  
1 5

&lt;210&gt; 94

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr  
1 5 10 15

Pro

&lt;210&gt; 95

&lt;211&gt; 14

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

<223> Description of Unknown Organism: General Target  
Sequence Recognized by Hairpin Ribozyme

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&lt;221&gt; modified\_base

&lt;222&gt; (1)..(3)

&lt;223&gt; Wherein N is G, U, C or A

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (5)

&lt;223&gt; Wherein N is G, U, C or A

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (9)..(14)

&lt;223&gt; Wherein N is G, U, C or A

<400> 95  
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<210> 96  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Amplification  
 Primer Design Based on EST Sequence GenBank  
 Accession Number AA281296

<400> 96  
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<210> 97  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Amplification  
 Primer Design Based on EST Sequence GenBank  
 Accession Number AA281296

<400> 97  
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<210> 98  
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<220>  
 <223> Description of Artificial Sequence: Amplification  
 Primer Design Based on EST Sequence GenBank  
 Accession Number AA281296

<400> 98  
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<210> 99  
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 <212> DNA  
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 Accession Number AA281296

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<210> 100  
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<212> DNA  
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<223> Description of Artificial Sequence: Synthesized  
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<212> DNA

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<210> 103

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<212> DNA

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<210> 104

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthesized

Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

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<210> 105  
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<210> 118  
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<210> 119  
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Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 121  
ctgatggagg tccgggcata g

21

<210> 122

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 122  
 cctccgaggc cgtgcagt

18

<210> 123  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 123  
 cacctcaagc tttctagatc agtccaggat ggtcttgaag tca

43

<210> 124  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 124  
 ggaaggcaaa ggagggcagg gcga

24

<210> 125  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 125  
 cacgaattcg gatccaagct tttttttttt tttttt

37

<210> 126  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 126  
 gggttgccga gggtgggc 18

<210> 127  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 127  
 gcagtggatga gccgagtcct g 21

<210> 128  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 128  
 cgactttgga ggtgccttca 20

<210> 129  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 129  
 gctggtgcag cgcggggacc 20

<210> 130  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 130

gaggtgcaga gcgactactc ca 22

<210> 131  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 131  
 gtctcacctc gaggtgaag 20

<210> 132  
 <211> 22  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 132  
 ggctgctcct gcgtttggtg ga 22

<210> 133  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 133  
 gccagagatg gagccaccc 19

<210> 134  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 134  
 ggggtggctcc atctctggc 19

<210> 135  
 <211> 21  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 135

ccgcacgctc atcttccacg t

21

<210> 136

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 136

gcttggggat gaagcggtc

19

<210> 137

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 137

cgctgagct gtactttgtc a

21

<210> 138

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 138

cacctcaagc tttctagatc agctagcggc ccagcccaac tcccct

46

<210> 139

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence

GenBank Accession Number AA281296

<400> 139  
gcagcacaca tgcgtgaaac ctgt

24

<210> 140  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 140  
gtgtcagaga tgacgcgcag gaa

23

<210> 141  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 141  
accacacatt gcctgtcctg agt

23

<210> 142  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 142  
actggatcct tgacaattaa tgcacgcggt cgtataatgt gtggagggtt gcggagggtg 60  
ggc 63

<210> 143  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 143  
ctgtaatacg actcactata gggttgcgga gggtgggc

38



<210> 144  
 <211> 73  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 144  
 cacctgcaga catgcgtttc gtcttcacgg actcatcagg ccagctggcg acgcatgtgt 60  
 gagccgagtc ctg 73

<210> 145  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 145  
 ggatccgccg cagagcaccg tctg

24

<210> 146  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 146  
 cgaagctttc agtgggccgg catctgaac

29

<210> 147  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 147  
 cgaagctttc acaggcccag cccaactcc

29

<210> 148  
 <211> 26  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 148

gcggatccag agccacgtcc tacgtc

26

<210> 149

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 149

gcggatccgt tcagatgccg gcccac

26

<210> 150

<211> 9

<212> PRT

<213> Homo sapiens

<400> 150

Pro Glu Met Glu Pro Pro Arg Arg Pro  
1 5

<210> 151

<211> 4

<212> PRT

<213> Homo sapiens

<400> 151

Ala Ala Glu His  
1

<210> 152

<211> 6

<212> PRT

<213> Homo sapiens

<400> 152

Val Gln Met Pro Ala His  
1 5

<210> 153

<211> 5

<212> PRT

<213> Homo sapiens

<400> 153  
Val Gly Leu Gly Leu  
1 5

<210> 154  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 154  
Arg Ala Thr Ser  
1

<210> 155  
<211> 622  
<212> PRT  
<213> Homo sapiens

<220>  
<223> N-Terminal Truncated Telomerase (ver.2); encoded  
by SEQ ID NO:51, with Y Intron ORF3

<400> 155  
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
1 5 10 15  
His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30  
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45  
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60  
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
65 70 75 80  
Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu  
85 90 95  
Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys  
100 105 110  
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
115 120 125  
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
130 135 140  
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
145 150 155 160  
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg

165										170					175				
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu				
			180					185					190						
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro				
		195					200					205							
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala				
	210					215					220								
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser				
225					230					235					240				
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg				
				245					250					255					
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro				
			260					265					270						
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly				
		275						280					285						
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe				
	290					295					300								
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu				
305					310					315					320				
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln				
				325					330					335					
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp				
			340					345					350						
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser				
		355					360					365							
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu				
	370					375					380								
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu				
385					390					395					400				
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu				
				405					410					415					
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly				
			420					425					430						
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro				
		435					440					445							
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys				
	450					455					460								
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg				

465

470

475

480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495

Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510

Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly  
 610 615 620

*sub D10*  
*19*  
*continued*